

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
- (ii) TITLE OF THE INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
- (iii) NUMBER OF SEQUENCES: 94
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036/2711
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: ON AN EVEN DATE HEREWITH
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/981,392
(B) FILING DATE: 22-DEC-1997
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Antler, Adriane M.
(B) REGISTRATION NUMBER: 32,605
(C) REFERENCE/DOCKET NUMBER: 7326-122
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-790-9090
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(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 277...2460

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA	CGAGGTTTTT	TTTTTTTTTT	TTCCCCTCTT	TTCTTTCTTT	TCCTTTTGCC	60										
ATCCGAAAGA	GCTGTCAGCC	GCCGCCGGGC	TGCACCTAAA	GGCGTCGGTA	GGGGGATAAC	120										
AGTCAGAGAC	CCTCCTGAAA	GCAGGAGACG	GGACGGTACC	CCTCCGGCTC	TGCGGGGCGG	180										
CTGCGGCCCC	TCCGTTCTTT	CCCCCTCCCC	GAGAGACACT	CTTCCTTTCC	CCCCACGAAG	240										
ACACAGGGGC	AGGAACGCGA	GCGCTGCCCC	TCCGCC	ATG	GGA GGC CGC TTC CTG	294										
			Met	Gly Gly Arg Phe Leu												
			1		5											
CTG	ACG	CTC	GCC	CTC	CTC	TCG	GCG	CTG	CTG	TGC	CGC	TGC	CAG	GTT	GAC	342
Leu	Thr	Leu	Ala	Leu	Leu	Ser	Ala	Leu	Leu	Cys	Arg	Cys	Gln	Val	Asp	
			10					15								20
GGC	TCC	GGG	GTG	TTC	GAG	CTG	AAG	CTG	CAG	GAG	TTT	GTC	AAC	AAG	AAG	390
Gly	Ser	Gly	Val	Phe	Glu	Leu	Lys	Leu	Gln	Glu	Phe	Val	Asn	Lys	Lys	
			25				30					35				
GGG	CTG	CTC	AGC	AAC	CGC	AAC	TGC	TGC	CGG	GGG	GGC	GGC	CCC	GGA	GGC	438
Gly	Leu	Leu	Ser	Asn	Arg	Asn	Cys	Cys	Arg	Gly	Gly	Gly	Pro	Gly	Gly	
			40				45									50
GCC	GGG	CAG	CAG	CAG	TGC	GAC	TGC	AAG	ACC	TTC	TTC	CGC	GTC	TGC	CTG	486
Ala	Gly	Gln	Gln	Gln	Cys	Asp	Cys	Lys	Thr	Phe	Phe	Arg	Val	Cys	Leu	
						60						65				70
AAG	CAC	TAC	CAG	GCC	AGC	GTC	TCC	CCC	GAG	CCG	CCC	TGC	ACC	TAC	GGC	534
Lys	His	Tyr	Gln	Ala	Ser	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr	Tyr	Gly	
						75						80				85
AGC	GCC	ATC	ACC	CCC	GTC	CTC	GGC	GCC	AAC	TCC	TTC	AGC	GTC	CCC	GAC	582
Ser	Ala	Ile	Thr	Pro	Val	Leu	Gly	Ala	Asn	Ser	Phe	Ser	Val	Pro	Asp	
						90										100
GGC	GCG	GGC	GGC	GCC	GAC	CCC	GCC	TTC	AGC	AAC	CCC	ATC	CGC	TTC	CCC	630
Gly	Ala	Gly	Gly	Ala	Asp	Pro	Ala	Phe	Ser	Asn	Pro	Ile	Arg	Phe	Pro	
						105										110
TTC	GGC	TTC	ACC	TGG	CCC	GGC	ACC	TTC	TCG	CTC	ATC	ATC	GAG	GCT	CTG	678
Phe	Gly	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Leu	
						120										125
CAC	ACC	GAC	TCC	CCC	GAC	GAC	CTC	ACC	ACA	GAA	AAC	CCC	GAG	CGC	CTC	726
His	Thr	Asp	Ser	Pro	Asp	Asp	Leu	Thr	Thr	Glu	Asn	Pro	Glu	Arg	Leu	
						135										140
ATC	AGC	CGC	CTG	GCC	ACC	CAG	AGG	CAC	CTG	GCG	GTG	GGC	GAG	GAG	TGG	774
Ile	Ser	Arg	Leu	Ala	Thr	Gln	Arg	His	Leu	Ala	Val	Gly	Glu	Glu	Trp	
																145
																150

	155					160					165					
TCC CAG GAC CTG CAC AGC AGC GGC CGC ACC GAC CTC AAG TAC TCC TAT	170					175					180					822
Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr																
CGC TTT GTG TGT GAT GAG CAC TAC TAC GGG GAA GGC TGC TCT GTC TTC	185					190					195					870
Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe																
TGC CGG CCC CGT GAC GAC CGC TTC GGT CAC TTC ACC TGT GGA GAG CGT	200					205					210					918
Cys Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg																
GGC GAG AAG GTC TGC AAC CCA GGC TGG AAG GGC CAG TAC TGC ACT GAG	215					220					225					966
Gly Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Gln Tyr Cys Thr Glu																
CCG ATT TGC TTG CCT GGG TGT GAC GAG CAG CAC GGC TTC TGC GAC AAA	235					240					245					1014
Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys																
CCT GGG GAA TGC AAG TGC AGA GTG GGT TGG CAG GGG CGG TAC TGT GAC	250					255					260					1062
Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp																
GAG TGC ATC CGA TAC CCA GGC TGC CTG CAC GGT ACC TGT CAG CAG CCA	265					270					275					1110
Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro																
TGG CAG TGC AAC TGC CAG GAA GGC TGG GGC GGC CTT TTC TGC AAC CAG	280					285					290					1158
Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln																
GAC CTG AAC TAC TGC ACT CAC CAC AAG CCA TGC AAG AAT GGT GCC ACA	295					300					305					1206
Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr																
TGC ACC AAC ACC GGT CAG GGG AGC TAC ACT TGT TCT TGC CGA CCT GGG	315					320					325					1254
Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly																
TAC ACA GGC TCC AGC TGC GAG ATT GAA ATC AAC GAA TGT GAT GCC AAC	330					335					340					1302
Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile Asn Glu Cys Asp Ala Asn																
CCT TGC AAG AAT GGT GGA AGC TGC ACG GAT CTC GAG AAC AGC TAT TCC	345					350					355					1350
Pro Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser																
TGT ACC TGC CCC CCA GGC TTC TAT GGT AAA AAC TGT GAG CTG AGT GCA	360					365					370					1398
Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Asn Cys Glu Leu Ser Ala																
ATG ACT TGT GCT GAT GGA CCG TGC TTC AAT GGA GGG CGA TGC ACT GAC	375					380					385					1446
Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Thr Asp																

AAC CCT GAT GGT GGA TAC AGC TGC CGC TGC CCA CTG GGT TAT TCT GGG	1494
Asn Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Leu Gly Tyr Ser Gly	
395 400 405	
TTC AAC TGT GAA AAG AAA ATC GAT TAC TGC AGT TCC AGC CCT TGT GCT	1542
Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ala	
410 415 420	
AAT GGA GCC CAG TGC GTT GAC CTG GGG AAC TCC TAC ATA TGC CAG TGC	1590
Asn Gly Ala Gln Cys Val Asp Leu Gly Asn Ser Tyr Ile Cys Gln Cys	
425 430 435	
CAG GCT GGC TTC ACT GGC AGG CAC TGT GAC GAC AAC GTG GAC GAT TGC	1638
Gln Ala Gly Phe Thr Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys	
440 445 450	
GCC TCC TTC CCC TGC GTC AAT GGA GGG ACC TGT CAG GAT GGG GTC AAC	1686
Ala Ser Phe Pro Cys Val Asn Gly Gly Thr Cys Gln Asp Gly Val Asn	
455 460 465 470	
GAC TAC TCC TGC ACC TGC CCC CCG GGA TAC AAC GGG AAG AAC TGC AGC	1734
Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr Asn Gly Lys Asn Cys Ser	
475 480 485	
ACG CCG GTG AGC AGA TGC GAG CAC AAC CCC TGC CAC AAT GGG GCC ACC	1782
Thr Pro Val Ser Arg Cys Glu His Asn Pro Cys His Asn Gly Ala Thr	
490 495 500	
TGC CAC GAG AGA AGC AAC CGC TAC GTG TGC GAG TGC GCT CGG GGC TAC	1830
Cys His Glu Arg Ser Asn Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr	
505 510 515	
GGC GGC CTC AAC TGC CAG TTC CTG CTC CCC GAG CCA CCT CAG GGG CCG	1878
Gly Gly Leu Asn Cys Gln Phe Leu Leu Pro Glu Pro Pro Gln Gly Pro	
520 525 530	
GTC ATC GTT GAC TTC ACC GAG AAG TAC ACA GAG GGC CAG AAC AGC CAG	1926
Val Ile Val Asp Phe Thr Glu Lys Tyr Thr Glu Gly Gln Asn Ser Gln	
535 540 545 550	
TTT CCC TGG ATC GCA GTG TGC GCC GGG ATT ATT CTG GTC CTC ATG CTG	1974
Phe Pro Trp Ile Ala Val Cys Ala Gly Ile Ile Leu Val Leu Met Leu	
555 560 565	
CTG CTG GGT TGC GCC GCC ATC GTC GTC TGC GTC AGG CTG AAG GTG CAG	2022
Leu Leu Gly Cys Ala Ala Ile Val Val Cys Val Arg Leu Lys Val Gln	
570 575 580	
AAG AGG CAC CAC CAG CCC GAG GCC TGC AGG AGT GAA ACG GAG ACC ATG	2070
Lys Arg His His Gln Pro Glu Ala Cys Arg Ser Glu Thr Glu Thr Met	
585 590 595	
AAC AAC CTG GCG AAC TGC CAG CGC GAG AAG GAC ATC TCC ATC AGC GTC	2118
Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Ile Ser Val	
600 605 610	
ATC GGT GCC ACT CAG ATT AAA AAC ACA AAT AAG AAA GTA GAC TTT CAC	2166
Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Val Asp Phe His	

615	620	625	630	
AGC GAT AAC TCC GAT AAA AAC GGC TAC AAA GTT AGA TAC CCA TCA GTG				2214
Ser Asp Asn Ser Asp Lys Asn Gly Tyr Lys Val Arg Tyr Pro Ser Val	635	640	645	
GAT TAC AAT TTG GTG CAT GAA CTC AAG AAT GAG GAC TCT GTG AAA GAG				2262
Asp Tyr Asn Leu Val His Glu Leu Lys Asn Glu Asp Ser Val Lys Glu	650	655	660	
GAG CAT GGC AAA TGC GAA GCC AAG TGT GAA ACG TAT GAT TCA GAG GCA				2310
Glu His Gly Lys Cys Glu Ala Lys Cys Glu Thr Tyr Asp Ser Glu Ala	665	670	675	
GAA GAG AAA AGC GCA GTA CAG CTA AAA AGT AGT GAC ACT TCT GAA AGA				2358
Glu Glu Lys Ser Ala Val Gln Leu Lys Ser Ser Asp Thr Ser Glu Arg	680	685	690	
AAA CGG CCA GAT TCA GTA TAT TCC ACT TCA AAG GAC ACA AAG TAC CAG				2406
Lys Arg Pro Asp Ser Val Tyr Ser Thr Ser Lys Asp Thr Lys Tyr Gln	695	700	705	710
TCG GTG TAC GTC ATA TCA GAA GAG AAA GAT GAG TGC ATC ATA GCA ACT				2454
Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Ile Ile Ala Thr	715	720	725	
GAG GTG TAAACAGAC GTGACGTGGC AAAGCTTATC GATACCGTCA TCAAGCTT				2508
Glu Val				

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Gly Arg Phe Leu Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu	
1 5 10 15	
Cys Arg Cys Gln Val Asp Gly Ser Gly Val Phe Glu Leu Lys Leu Gln	
20 25 30	
Glu Phe Val Asn Lys Lys Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg	
35 40 45	
Gly Gly Gly Pro Gly Gly Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr	
50 55 60	
Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser Pro Glu	
65 70 75 80	
Pro Pro Cys Thr Tyr Gly Ser Ala Ile Thr Pro Val Leu Gly Ala Asn	
85 90 95	
Ser Phe Ser Val Pro Asp Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser	
100 105 110	
Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser	

Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Thr Thr
 130 135 140
 Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu
 145 150 155 160
 Ala Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr
 165 170 175
 Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly
 180 185 190
 Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Arg Phe Gly His
 195 200 205
 Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys
 210 215 220
 Gly Gln Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln
 225 230 235 240
 His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp
 245 250 255
 Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His
 260 265 270
 Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly
 275 280 285
 Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro
 290 295 300
 Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr
 305 310 315 320
 Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile
 325 330 335
 Asn Glu Cys Asp Ala Asn Pro Cys Lys Asn Gly Gly Ser Cys Thr Asp
 340 345 350
 Leu Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys
 355 360 365
 Asn Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn
 370 375 380
 Gly Gly Arg Cys Thr Asp Asn Pro Asp Gly Gly Tyr Ser Cys Arg Cys
 385 390 395 400
 Pro Leu Gly Tyr Ser Gly Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys
 405 410 415
 Ser Ser Ser Pro Cys Ala Asn Gly Ala Gln Cys Val Asp Leu Gly Asn
 420 425 430
 Ser Tyr Ile Cys Gln Cys Gln Ala Gly Phe Thr Gly Arg His Cys Asp
 435 440 445
 Asp Asn Val Asp Asp Cys Ala Ser Phe Pro Cys Val Asn Gly Gly Thr
 450 455 460
 Cys Gln Asp Gly Val Asn Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr
 465 470 475 480
 Asn Gly Lys Asn Cys Ser Thr Pro Val Ser Arg Cys Glu His Asn Pro
 485 490 495
 Cys His Asn Gly Ala Thr Cys His Glu Arg Ser Asn Arg Tyr Val Cys
 500 505 510
 Glu Cys Ala Arg Gly Tyr Gly Gly Leu Asn Cys Gln Phe Leu Leu Pro
 515 520 525
 Glu Pro Pro Gln Gly Pro Val Ile Val Asp Phe Thr Glu Lys Tyr Thr
 530 535 540
 Glu Gly Gln Asn Ser Gln Phe Pro Trp Ile Ala Val Cys Ala Gly Ile
 545 550 555 560
 Ile Leu Val Leu Met Leu Leu Leu Gly Cys Ala Ala Ile Val Val Cys
 565 570 575

Val Arg Leu Lys Val Gln Lys Arg His His Gln Pro Glu Ala Cys Arg
580 585 590
Ser Glu Thr Glu Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys
595 600 605
Asp Ile Ser Ile Ser Val Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn
610 615 620
Lys Lys Val Asp Phe His Ser Asp Asn Ser Asp Lys Asn Gly Tyr Lys
625 630 635 640
Val Arg Tyr Pro Ser Val Asp Tyr Asn Leu Val His Glu Leu Lys Asn
645 650 655
Glu Asp Ser Val Lys Glu Glu His Gly Lys Cys Glu Ala Lys Cys Glu
660 665 670
Thr Tyr Asp Ser Glu Ala Glu Glu Lys Ser Ala Val Gln Leu Lys Ser
675 680 685
Ser Asp Thr Ser Glu Arg Lys Arg Pro Asp Ser Val Tyr Ser Thr Ser
690 695 700
Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Ile Ser Glu Glu Lys Asp
705 710 715 720
Glu Cys Ile Ile Ala Thr Glu Val
725

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCA	CGAGGTTTTT	TTTTTTTTTT	TTCCCCTCTT	TTCTTTCTTT	TCCTTTTGCC	60
ATCCGAAAGA	GCTGTCAGCC	GCCGCCGGGC	TGCACCTAAA	GGCGTCGGTA	GGGGGATAAC	120
AGTCAGAGAC	CCTCCTGAAA	GCAGGAGACG	GGACGGTACC	CCTCCGGCTC	TGCGGGGCGG	180
CTGCGGCCCC	TCCGTTCTTT	CCCCCTCCCC	GAGAGACACT	CTTCCTTTCC	CCCCACGAAG	240
ACACAGGGGC	AGGAACGCGA	GCGCTGCCCC	TCCGCCATGG	GAGGCCGCTT	CCTGCTGACG	300
CTCGCCCTCC	TCTCGGCGCT	GCTGTGCCGC	TGCCAGGTTG	ACGGCTCCGG	GGTGTTCGAG	360
CTGAAGCTGC	AGGAGTTTGT	CAACAAGAAG	GGGCTGCTCA	GCAACCGCAA	CTGCTGCCGG	420
GGGGGCGGCC	CCGGAGGCGC	CGGGCAGCAG	CAGTGC GACT	GCAAGACCTT	CTTCCGCGTC	480
TGCCCTGAAGC	ACTACCAGGC	CAGCGTCTCC	CCCAGGCCGC	CCTGCACCTA	CGGCAGCGCC	540
ATCACCCCG	TCCTCGGCGC	CAACTCCTTC	AGCGTCCCCG	ACGGCGCGGG	CGGCGCCGAC	600
CCCGCCTTCA	GCAACCCCAT	CCGCTTCCCC	TTCGGCTTCA	CCTGGCCCGG	CACCTTCTCG	660
CTCATCATCG	AGGCTCTGCA	CACCGACTCC	CCCGACGACC	TCACCACAGA	AAACCCCGAG	720
CGCCTCATCA	GCCGCCTGGC	CACCCAGAGG	CACCTGGCGG	TGGGCGAGGA	GTGGTCCCAG	780
GACCTGCACA	GCAGCGGCCG	CACCGACCTC	AAGTACTCCT	ATCGCTTTGT	GTGTGATGAG	840
CACTACTACG	GGGAAGGCTG	CTCTGTCTTC	TGCCGGCCCC	GTGACGACCG	CTTCGGTCAC	900
TTACCTGTG	GAGAGCGTGG	CGAGAAGGTC	TGCAACCCAG	GCTGGAAGGG	CCAGTACTGC	960
ACTGAGCCGA	TTTGCTTGCC	TGGGTGTGAC	GAGCAGCACG	GCTTCTGCGA	CAAACCTGGG	1020
GAATGCAAGT	GCAGAGTGGG	TTGGCAGGGG	CGGTACTGTG	ACGAGTGCAT	CCGATACCCA	1080
GGCTGCCTGC	ACGGTACCTG	TCAGCAGCCA	TGGCAGTGCA	ACTGCCAGGA	AGGCTGGGGC	1140
GGCCTTTTCT	GCAACCAGGA	CCTGAACTAC	TGCACTCACC	ACAAGCCATG	CAAGAATGGT	1200
GCCACATGCA	CCAACACCGG	TCAGGGGAGC	TACACTTGTT	CTTGCCGACC	TGGGTACACA	1260
GGCTCCAGCT	GCGAGATTGA	AATCAACGAA	TGTGATGCCA	ACCCTTGCAA	GAATGGTGGA	1320
AGCTGCACGG	ATCTCGAGAA	CAGCTATTCC	TGTACCTGCC	CCCCAGGCTT	CTATGGTAAA	1380
AACTGTGAGC	TGAGTGCAAT	GACTTGTGCT	GATGGACCGT	GCTTCAATGG	AGGGCGATGC	1440
ACTGACAACC	CTGATGGTGG	ATACAGCTGC	CGCTGCCCAC	TGGGTTATTC	TGGGTTCAAC	1500

TGTGAAAAGA	AAATCGATTA	CTGCAGTICC	AGCCCTTGTG	CTAATGGAGC	CCAGTGCCTT	1560
GACCTGGGGA	ACTCCTACAT	ATGCCAGTGC	CAGGCTGGCT	TCACTGGCAG	GCACTGTGAC	1620
GACAACGTGG	ACGATTGCGC	CTCCTTCCCC	TGCGTCAATG	GAGGGACCTG	TCAGGATGGG	1680
GTCAACGACT	ACTCCTGCAC	CTGCCCCCGG	GGATACAACG	GGAAGAACTG	CAGCACGCCG	1740
GTGAGCAGAT	GCGAGCACAA	CCCCTGCCAC	AATGGGGCCA	CCTGCCACGA	GAGAAGCAAC	1800
CGCTACGTGT	GCGAGTGC	TCGGGGCTAC	GGCGGCCTCA	ACTGCCAGTT	CCTGCTCCCC	1860
GAGCCACCTC	AGGGGCCGGT	CATCGTTGAC	TTCACCGAGA	AGTACACAGA	GGGCCAGAAC	1920
AGCCAGTTTC	CCTGGATCGC	AGTGTGCGCC	GGGATTATTC	TGGTCCTCAT	GCTGCTGCTG	1980
GGTTGCGCCG	CCATCGTCGT	CTGCGTCAGG	CTGAAGGTGC	AGAAGAGGCA	CCACCAGCCC	2040
GAGGCCTGCA	GGAGTGAAAC	GGAGACCATG	AACAACCTGG	CGAACTGCCA	GCGCGAGAAG	2100
GACATCTCCA	TCAGCGTCAT	CGGTGCCACT	CAGATTAAAA	ACACAAATAA	GAAAGTAGAC	2160
TTTCACAGCG	ATAACTCCGA	TAAAAACGGC	TACAAAGTTA	GATACCCATC	AGTGGATTAC	2220
AATTTGGTGC	ATGAAC TCA	GAATGAGGAC	TCTGTGAAAG	AGGAGCATGG	CAAATGCGAA	2280
GCCAAGTGTG	AAACGTATGA	TTCAGAGGCA	GAAGAGAAAA	GCGCAGTACA	GCTAAAAAGT	2340
AGTGACACTT	CTGAAAGAAA	ACGGCCAGAT	TCAGTATATT	CCACTTCAAA	GGACACAAAG	2400
TACCAGTCGG	TGTACGTCAT	ATCAGAAGAG	AAAGATGAGT	GCATCATAGC	AACTGAGGTT	2460
AGTATCCAC	CTGGCAGTCG	GACAAGTCTT	GGTGTGTGAT	TCCCATCCAG	CGCAGGTCAG	2520
GGCGGCCAAA	CCATTCTACC	TGCTGCCACA	GTCATCTGTA	CCCAATGAAA	ACTGGCCACC	2580
TTCAGTCTGT	GGCACTGCAG	ACGTTGAAAA	AACTTGTGTG	GGATTAACAT	AAGCTCCAGT	2640
GGGGGTTACA	GGGACAGCAA	TTTTTGCAGG	CAAGGGTATA	ACTGTAGTGC	AGTTGTAGCT	2700
TACTAACCCT	ACTGACTCAT	TCTTTCGTGT	GCTTCCGTGCA	GAGCCTGTTT	TTGCTTGGCA	2760
TTGAGGTGAA	GTCCTGACCC	TCTGCATCCT	CATAGTCCTC	TGCTTCTTTT	TTATTAACCT	2820
CTTCTGGTCT	CTGCTTGTCT	TTTCTCTCAA	CAGGTGTAAA	ACAGACGTGA	CGTGGCAAAG	2880
CTT						2883

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCCAGCGGT	ACCATGGGCC	GTCGGAGCGC	GCTACCCCTT	GCCGTGGTCT	CTGCCCTGCT	60
GTGCCAGGTC	TGGAGCTCCG	GCGTATTTGA	GCTGAAGCTG	CAGGAGTTCG	TCAACAAGAA	120
GGGGCTGCTG	GGGAACCGCA	ACTGCTGCCG	CGGGGGCTCT	GGCCCGCCTT	GCGCCTGCAG	180
GACCTTCTTT	CGCGTATGCC	TCAACCACTA	CCAGGCCAGC	GTGTCACCGG	AGCCACCCTG	240
CACCTACGGC	AGTGCTGTCA	CGCCAGTGCT	GGGTCTCGAC	TCCTTCAGCC	TGCCTGATGG	300
CGCAGGCATC	GACCCCGCCT	TCAGCAACCC	ATCCGATTCC	CCTTCCGGCT	TCACCTGGCC	360
AGGTACCTTC	TCTCTGATCA	TTGAAGCCCT	CCATACAGAC	TCTCCCGATG	ACCTCGCAAC	420
AGAAAACCCA	GAAAGACTCA	TCAGCCGCCT	GACCACACAG	AGGCACCTCA	CTGTGGGACG	480
AATGGTCTCA	GGACCTTCAC	AGTAGCGGCC	GCACAGACCT	CCGGTACTCT	TACCGGTTTG	540
TGTGTGACGA	GCACTACTAC	GGAGAAGGTT	GCTCTGTGTT	CTGCCGACCT	CGGGATGACG	600
CCTTTGGCCA	CTTCACCTGC	GGGGACAGAG	GGGAGAAGAT	GTGCGACCCCT	GGCTGGAAAG	660
GCCAGTACTG	CACTGACCCA	ATCTGTCTGC	CAGGGTGTGA	TGACCAACAT	GGATACTGTG	720
ACAAACCAGG	GGAGTGCAAG	TGCAGAGTTG	GCTGGCAGGG	CCGCTACTGC	GATGAGTGCA	780
TCCGATACCC	AGGTTGTCTC	CATGGCACCT	GCCAGCAACC	CTGGCAGTGT	AACTGCCAGG	840
AAGGCTGGGG	GGGCCTTTTC	TGCAACCAAG	ACCTGAACTA	CTGTACTCAC	CATAAGCCGT	900
GCAGGAATGG	AGCCACCTGC	ACCAACACGG	GCCAGGGGAG	CTACACATGT	TCCTGCCGAC	960
TGGGGTATAC	AGGTGCCAAC	TGTGAGCTGG	AAGTAGATGA	GTGTGCTCCT	AGCCCTTGCA	1020
AGAACGGAGC	GAGCTGCACG	GACCTTGAGG	ACAGCTTCTC	TTGCACCTGC	CCTCCCGGCT	1080
TCTATGGCAA	GGTCTGTGAG	CTTGAGCGCC	ATGACCTGTG	CAGATGGCCC	TTGCTTCAAT	1140
GGAGGACGAT	GTTCAGATAA	CCCTGACGGA	GGCTACACCT	GCCATTGCCC	CTTGGGCTTC	1200
TCTGGCTTCA	ACTGTGAGAA	GAAGATGGAT	CTCTGCGGCT	CTTCCCCCTT	GTTCTAACGG	1260

TGCCAAGTGT	GTGGACCTCG	GCAACTCTTA	CCTGTGCCGG	TGCCAGGCTG	GCTTCTCCGG	1320
GACCTACTGC	GAGGACAATG	TGGATGACTG	TGCCTCCTCC	CCGTGTGCAA	ATGGGGGCAC	1380
CTGCCGGGAC	AGTGTGAACG	ACTTCTCCTC	TACCTGCCCA	CCTGGCTACA	CGGGCAAGAA	1440
CTGCAGCGCC	CCTGTCAGCA	GGTGTGAGCA	TGCACCCTGC	CATAATGGGG	CCACCTGCCA	1500
CCAGAAGGGC	CAGCGCTACA	TGTGTGAGTG	CGCCCAGGGC	TATGGCGGGC	CCAACTGCCA	1560
GTTTCTGCTC	CCTGAGCCAC	CACCAGGGCC	CATGGTGGTG	GACCTCAGTG	AGAGGCATAT	1620
GGAGAGCCAG	GGCGGGCCCT	TCCCCTCGGT	GGCGGTGTGT	GCCGGGGTGG	TGCTTGTCTT	1680
CCTGCTGCTG	CTGGGCTGTG	CTGCTGTGGT	GGTCTGCGTC	CGGCTGAAGC	TACAGAAACA	1740
CCAGCCTCCA	CCTGAACCCT	GTGGGGGAGA	GACAGAAACC	ATGAACAACC	TAGCCAATTG	1800
CCAGCGCGAG	AAGGACGTTT	CTGTTAGCAT	CATTGGGGCT	ACCCAGATCA	AGAACACCAA	1860
CAAGAAGGCG	GACTTTTACG	GGGACCATGG	AGCCAAGAAG	AGCAGCTTTA	AGGTCCGATA	1920
CCCCACTGTG	GACTATAACC	TCGTTTCGAGA	CCTCAAGGGA	GATGAAGCCA	CGGTCAGGGA	1980
TACACACAGC	AAACGTGACA	CCAAGTGCCA	GTCACAGAGC	TCTGCAGGAG	AAGAGAAGAT	2040
CGCCCCAACA	CTTAGGGGTG	GGGAGATTCC	TGACAGAAAA	AGGCCAGAGT	CTGTCTACTC	2100
TACTTCAAAG	GACACCAAGT	ACCAGTCGGT	GTATGTTCTG	TCTGCAGAAA	AGGATGAGTG	2160
TGTTATAGCG	ACTGAGCTGT	AAGATGGAAG	CGATGTGGCA	AAATTCCTAT	TTCTCTCAAA	2220
TAAAATTCCA	AGGATATAGC	CCCGATGAAT	GCTGCTGAGA	GAGGAAGGGA	GAGGAAACCC	2280
AGGGACTGCT	GCTGAGAACC	AGGTTTCAGG	GAAGCTGGTT	CTCTCAGAGT	TAGCAGAGGC	2340
GCCCGACACT	GCCAGCCTAG	GCTTTGGCTG	CCGCTGGACT	GCCTGCTGGT	TGTTCCCATT	2400
GCACTATGGA	CAGTTGCTTT	GAAGAGTATA	TATTTAAATG	GACGAGTGAC	TTGATTGATA	2460
TACGAAGCAC	GCACTGCCCA	CACGTCATAT	TTGGATTACT	ATGAGCCAGT	CTTTCCTTGA	2520
ACTAGAAACA	CAACTGCCTT	TATTGTCCTT	TTTGATACTG	AGATGTGTTT	TTTTTTTTTC	2580
TAGACGGGAA	AAAGAAAACG	TGTGTTATTT	TTTTGGGATT	TGTAAAAATA	TTTTTTCATG	2640
TATCTGTAAA	GCTTGAGTAT	TTTGTGACGT	TCATTTTTTT	ATAATTTAAA	TTTTGGTAAA	2700
TATGTACAAA	GGCACTTCGG	GTCTATGTGA	CTATATTTTT	TTGTATATAA	ATGTATTTAT	2760
GGAATATTGT	GCAAATGTTA	TTTGAGTTTT	TTACTGTTTT	GTTAATGAAG	AAATTCATTT	2820
TAAAAATATT	TTTCCAAAAT	AAATATAATG	AACTACA			2857

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Gly	Gln	Gln	Arg	Met	Leu	Thr	Leu	Leu	Val	Leu	Ser	Ala	Val	Leu
1				5				10						15	
Cys	Gln	Ile	Ser	Cys	Ser	Gly	Leu	Phe	Glu	Leu	Arg	Leu	Gln	Glu	Phe
			20					25					30		
Val	Asn	Lys	Lys	Gly	Leu	Leu	Gly	Asn	Met	Asn	Cys	Cys	Arg	Pro	Gly
		35					40					45			
Ser	Leu	Ala	Ser	Leu	Gln	Arg	Cys	Glu	Cys	Lys	Thr	Phe	Phe	Arg	Ile
		50				55				60					
Cys	Leu	Lys	His	Tyr	Gln	Ser	Asn	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr
65					70					75				80	
Tyr	Gly	Gly	Ala	Val	Thr	Pro	Val	Leu	Gly	Thr	Asn	Ser	Phe	Val	Val
			85						90					95	
Pro	Glu	Ser	Ser	Asn	Ala	Asp	Pro	Thr	Phe	Ser	Asn	Pro	Ile	Arg	Phe
			100					105					110		
Pro	Phe	Gly	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala
		115					120					125			
Ile	His	Ala	Asp	Ser	Ala	Asp	Asp	Leu	Asn	Thr	Glu	Asn	Pro	Glu	Arg
	130					135					140				

Gly	Thr	Thr	Gln	Ile	Lys	Asn	Thr	Asn	Lys	Lys	Ile	Asp	Phe	Leu	Ser
610						615					620				
Glu	Ser	Asn	Asn	Glu	Lys	Asn	Gly	Tyr	Lys	Pro	Arg	Tyr	Pro	Ser	Val
625					630					635					640
Asp	Tyr	Asn	Leu	Val	His	Glu	Leu	Lys	Asn	Glu	Asp	Ser	Pro	Lys	Glu
				645					650					655	
Glu	Arg	Ser	Lys	Cys	Glu	Ala	Lys	Cys	Ser	Ser	Asn	Asp	Ser	Asp	Ser
			660					665					670		
Glu	Asp	Val	Asn	Ser	Val	His	Ser	Lys	Arg	Asp	Ser	Ser	Glu	Arg	Arg
		675					680					685			
Arg	Pro	Asp	Ser	Ala	Tyr	Ser	Thr	Ser	Lys	Asp	Thr	Lys	Tyr	Gln	Ser
	690					695					700				
Val	Tyr	Val	Ile	Ser	Asp	Glu	Lys	Asp	Glu	Cys	Ile	Ile	Ala	Thr	Glu
705					710					715					720
Val															

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	His	Trp	Ile	Lys	Cys	Leu	Leu	Thr	Ala	Phe	Ile	Cys	Phe	Thr	Val
1				5					10					15	
Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	Glu	Leu	Arg	Leu	Lys	Tyr
		20						25					30		
Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	Gly	Arg	Cys	Cys	Ser	Gly
		35				40						45			
Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	Gly	Ser	Cys	Lys	Thr	Arg
		50				55					60				
Phe	Arg	Leu	Cys	Leu	Lys	His	Tyr	Gln	Ala	Thr	Ile	Asp	Thr	Thr	Ser
65					70					75					80
Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	Ile	Leu	Gly	Glu	Asn	Ser
			85					90						95	
Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	Asn	Lys	Gly	Phe	Thr	Asn
		100						105					110		
Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	Pro	Gly	Thr	Phe	Ser	Leu
		115					120					125			
Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	Ser	Gly	Asn	Ala	Arg	Thr
		130				135					140				
Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	Gln	Gln	Val	Leu	Glu	Val
145					150					155					160
Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	Ser	Gln	Tyr	Thr	Ser	Leu
			165					170						175	
Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	Asn	Tyr	Tyr	Gly	Ser	Gly
		180					185						190		
Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Ser	Phe	Gly	His	Ser	Thr
		195					200					205			
Cys	Ser	Glu	Thr	Gly	Glu	Ile	Ile	Cys	Leu	Thr	Gly	Trp	Gln	Gly	Asp
210						215					220				

Tyr Cys His Ile Pro Lys Cys Ala Lys Gly Cys Glu His Gly His Cys
 225 230 235 240
 Asp Lys Pro Asn Gln Cys Val Cys Gln Leu Gly Trp Lys Gly Ala Leu
 245 250 255
 Cys Asn Glu Cys Val Leu Glu Pro Asn Cys Ile His Gly Thr Cys Asn
 260 265 270
 Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly Trp Gly Gly Leu Tyr Cys
 275 280 285
 Asn Gln Asp Leu Asn Tyr Cys Thr Asn His Arg Pro Cys Lys Asn Gly
 290 295 300
 Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu Tyr Thr Cys Lys Cys Ala
 305 310 315 320
 Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn Glu Ile Tyr Ser Cys Asp
 325 330 335
 Ala Asp Val Asn Pro Cys Gln Asn Gly Gly Thr Cys Ile Asp Glu Pro
 340 345 350
 His Thr Lys Thr Gly Tyr Lys Cys His Cys Arg Asn Gly Trp Ser Gly
 355 360 365
 Lys Met Cys Glu Glu Lys Val Leu Thr Cys Ser Asp Lys Pro Cys His
 370 375 380
 Gln Gly Ile Cys Arg Asn Val Arg Pro Gly Leu Gly Ser Lys Gly Gln
 385 390 395 400
 Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr Ser Gly Pro Asn Cys Asp
 405 410 415
 Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro Cys Ile Asn Gly Gly Ser
 420 425 430
 Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro Ser Gly Phe Ser Gly Thr
 435 440 445
 Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu Gly His Gln Cys Glu Asn
 450 455 460
 Gly Gly Thr Cys Ile Asp Met Val Asn Gln Tyr Arg Cys Gln Cys Val
 465 470 475 480
 Pro Gly Phe His Gly Thr His Cys Ser Ser Lys Val Asp Leu Cys Leu
 485 490 495
 Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys Leu Asn Leu Asn Asn Asp
 500 505 510
 Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr Gly Lys Asp Cys Ser Val
 515 520 525
 Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys His Asn Gly Gly Thr Cys
 530 535 540
 Met Asn Arg Val Asn Ser Phe Glu Cys Val Cys Ala Asn Gly Phe Arg
 545 550 555 560
 Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp Ser Val Thr Phe Asp Ala
 565 570 575
 His Gln Tyr Gly Ala Thr Thr Gln Ala Arg Ala Asp Gly Leu Ala Asn
 580 585 590
 Ala Gln Val Val Leu Ile Ala Val Phe Ser Val Ala Met Pro Leu Val
 595 600 605
 Ala Val Ile Ala Ala Cys Val Val Phe Cys Met Lys Arg Lys Arg Lys
 610 615 620
 Arg Ala Gln Glu Lys Asp Asn Ala Glu Ala Arg Lys Gln Asn Glu Gln
 625 630 635 640
 Asn Ala Val Ala Thr Met His His Asn Gly Ser Ala Val Gly Val Ala
 645 650 655
 Leu Ala Ser Ala Ser Met Gly Gly Lys Thr Gly Ser Asn Ser Gly Leu
 660 665 670
 Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile Lys Asn Thr Trp Asp Lys
 675 680 685

Ser Val Asn Asn Ile Cys Ala Ser Ala Ala Ala Ala Ala Ala Ala
690 695 700
Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly Gly Tyr Val Ala Ser Val
705 710 715 720
Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe Cys Val Ala Pro Leu Gln
725 730 735
Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr Asp Pro Thr Leu Met His
740 745 750
Arg Gly Ser Pro Ala Gly Thr Ser Ala Lys Gly Ala Ser Gly Gly Gly
755 760 765
Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser Val Leu Gly Glu Gly Ser
770 775 780
Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala Ala Ala Gly Val Ala Gly
785 790 795 800
Asp Leu Phe Ile Gln Leu Met Ala Ala Ala Ser Val Ala Gly Thr Asp
805 810 815
Gly Thr Ala Gln Gln Gln Arg Ser Val Val Cys Gly Thr Pro His Met
820 825 830

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Gln Cys Ala Val Thr Tyr Tyr Asn Thr Thr Phe Cys Thr Thr Phe
1 5 10 15
Cys Arg Pro Arg Asp Asp Gln Phe Gly His Tyr Ala Cys Gly Ser Glu
20 25 30
Gly Gln Lys Leu Cys Leu Asn Gly Trp Gln Gly Val Asn Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Thr Cys Ala Glu His Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
1 5 10 15
Arg Pro Arg Asp Phe Phe Thr His Thr Cys Asp Gln Asn Gly
20 25 30
Asn Lys Thr Cys Leu Glu Gly Trp Thr Gly Pro Glu Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Asn Leu Cys Ser Ser Asn Tyr His Gly Lys Arg Cys Asn Arg Tyr Cys
 1             5             10             15
Ile Ala Asn Ala Lys Leu His Trp Glu Cys Ser Thr His Gly Val Arg
      20             25             30
Arg Cys Ser Ala Gly Trp Ser Gly Glu Asp Cys
      35             40
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Val Thr Cys Ala Arg Asn Tyr Phe Gly Asn Arg Cys Glu Asn Phe Cys
 1             5             10             15
Asp Ala His Leu Ala Lys Ala Ala Arg Lys Arg Cys Asp Ala Met Gly
      20             25             30
Arg Leu Arg Cys Asp Ile Gly Trp Met Gly Pro His Cys
      35             40             45
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...2199
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCC ATG GGC CGT CGG AGC GCG CTA      54
      Met Gly Arg Arg Ser Ala Leu
      1             5
```

GCC CTT GCC GTG GTC TCT GCC CTG CTG TGC CAG GTC TGG AGC TCC GGC	102
Ala Leu Ala Val Val Ser Ala Leu Leu Cys Gln Val Trp Ser Ser Gly	
10 15 20	
GTA TTT GAG CTG AAG CTG CAG GAG TTC GTC AAC AAG AAG GGG CTG CTG	150
Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly Leu Leu	
25 30 35	
GGG AAC CGC AAC TGC TGC CGC GGG GGC TCT GGC CCG CCT TGC GCC TGC	198
Gly Asn Arg Asn Cys Cys Arg Gly Gly Ser Gly Pro Pro Cys Ala Cys	
40 45 50 55	
AGG ACC TTC TTT CGC GTA TGC CTC AAG CAC TAC CAG GCC AGC GTG TCA	246
Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser	
60 65 70	
CCG GAG CCA CCC TGC ACC TAC GGC AGT GCC GTC ACG CCA GTG CTG GGT	294
Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro Val Leu Gly	
75 80 85	
GTC GAC TCC TTC AGC CTG CCT GAT GGC GCA GGC ATC GAC CCC GCC TTC	342
Val Asp Ser Phe Ser Leu Pro Asp Gly Ala Gly Ile Asp Pro Ala Phe	
90 95 100	
AGC AAC CCC ATC CGA TTC CCC TTC GGC TTC ACC TGG CCA GGT ACC TTC	390
Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe	
105 110 115	
TCT CTG ATC ATT GAA GCC CTC CAT ACA GAC TCT CCC GAT GAC CTC GCA	438
Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Ala	
120 125 130 135	
ACA GAA AAC CCA GAA AGA CTC ATC AGC CGC CTG ACC ACA CAG AGG CAC	486
Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Thr Thr Gln Arg His	
140 145 150	
CTC ACT GTG GGA GAA GAA TGG TCT CAG GAC CTT CAC AGT AGC GGC CGC	534
Leu Thr Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg	
155 160 165	
ACA GAC CTC CGG TAC TCT TAC CGG TTT GTG TGT GAC GAG CAC TAC TAC	582
Thr Asp Leu Arg Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr	
170 175 180	
GGA GAA GGT TGC TCT GTG TTC TGC CGA CCT CGG GAT GAC GCC TTT GGC	630
Gly Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Ala Phe Gly	
185 190 195	
CAC TTC ACC TGC GGG GAC AGA GGG GAG AAG ATG TGC GAC CCT GGC TGG	678
His Phe Thr Cys Gly Asp Arg Gly Glu Lys Met Cys Asp Pro Gly Trp	
200 205 210 215	
AAA GGC CAG TAC TGC ACT GAC CCA ATC TGT CTG CCA GGG TGT GAT GAC	726
Lys Gly Gln Tyr Cys Thr Asp Pro Ile Cys Leu Pro Gly Cys Asp Asp	
220 225 230	

CAA CAT GGA TAC TGT GAC AAA CCA GGG GAG TGC AAG TGC AGA GTT GGC	774
Gln His Gly Tyr Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly	
235 240 245	
TGG CAG GGC CGC TAC TGC GAT GAG TGC ATC CGA TAC CCA GGT TGT GTC	822
Trp Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Val	
250 255 260	
CAT GGC ACC TGC CAG CAA CCC TGG CAG TGT AAC TGC CAG GAA GGC TGG	870
His Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp	
265 270 275	
GGG GGC CTT TTC TGC AAC CAA GAC CTG AAC TAC TGT ACT CAC CAT AAG	918
Gly Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys	
280 285 290 295	
CCG TGC AGG AAT GGA GCC ACC TGC ACC AAC ACG GGC CAG GGG AGC TAC	966
Pro Cys Arg Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr	
300 305 310	
ACA TGT TCC TGC CGA CCT GGG TAT ACA GGT GCC AAC TGT GAG CTG GAA	1014
Thr Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ala Asn Cys Glu Leu Glu	
315 320 325	
GTA GAT GAG TGT GCT CCT AGC CCC TGC AAG AAC GGA GCG AGC TGC ACG	1062
Val Asp Glu Cys Ala Pro Ser Pro Cys Lys Asn Gly Ala Ser Cys Thr	
330 335 340	
GAC CTT GAG GAC AGC TTC TCT TGC ACC TGC CCT CCC GGC TTC TAT GGC	1110
Asp Leu Glu Asp Ser Phe Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly	
345 350 355	
AAG GTC TGT GAG CTG AGC GCC ATG ACC TGT GCA GAT GGC CCT TGC TTC	1158
Lys Val Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe	
360 365 370 375	
AAT GGA GGA CGA TGT TCA GAT AAC CCT GAC GGA GGC TAC ACC TGC CAT	1206
Asn Gly Gly Arg Cys Ser Asp Asn Pro Asp Gly Gly Tyr Thr Cys His	
380 385 390	
TGC CCC TTG GGC TTC TCT GGC TTC AAC TGT GAG AAG AAG ATG GAT CTC	1254
Cys Pro Leu Gly Phe Ser Gly Phe Asn Cys Glu Lys Lys Met Asp Leu	
395 400 405	
TGC GGC TCT TCC CCT TGT TCT AAC GGT GCC AAG TGT GTG GAC CTC GGC	1302
Cys Gly Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val Asp Leu Gly	
410 415 420	
AAC TCT TAC CTG TGC CGG TGC CAG GCT GGC TTC TCC GGG AGG TAC TGC	1350
Asn Ser Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly Arg Tyr Cys	
425 430 435	
GAG GAC AAT GTG GAT GAC TGT GCC TCC TCC CCG TGT GCA AAT GGG GGC	1398
Glu Asp Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala Asn Gly Gly	
440 445 450 455	

ACC TGC CGG GAC AGT GTG AAC GAC TTC TCC TGT ACC TGC CCA CCT GGC	1446
Thr Cys Arg Asp Ser Val Asn Asp Phe Ser Cys Thr Cys Pro Pro Gly	
460 465 470	
TAC ACG GGC AAG AAC TGC AGC GCC CCT GTC AGC AGG TGT GAG CAT GCA	1494
Tyr Thr Gly Lys Asn Cys Ser Ala Pro Val Ser Arg Cys Glu His Ala	
475 480 485	
CCC TGC CAT AAT GGG GCC ACC TGC CAC CAG AGG GGC CAG CGC TAC ATG	1542
Pro Cys His Asn Gly Ala Thr Cys His Gln Arg Gly Gln Arg Tyr Met	
490 495 500	
TGT GAG TGC GCC CAG GGC TAT GGC GGC CCC AAC TGC CAG TTT CTG CTC	1590
Cys Glu Cys Ala Gln Gly Tyr Gly Gly Pro Asn Cys Gln Phe Leu Leu	
505 510 515	
CCT GAG CCA CCA CCA GGG CCC ATG GTG GTG GAC CTC AGT GAG AGG CAT	1638
Pro Glu Pro Pro Pro Gly Pro Met Val Val Asp Leu Ser Glu Arg His	
520 525 530 535	
ATG GAG AGC CAG GGC GGG CCC TTC CCC TGG GTG GCC GTG TGT GCC GGG	1686
Met Glu Ser Gln Gly Gly Pro Phe Pro Trp Val Ala Val Cys Ala Gly	
540 545 550	
GTG GTG CTT GTC CTC CTG CTG CTG CTG GGC TGT GCT GCT GTG GTG GTC	1734
Val Val Leu Val Leu Leu Leu Leu Gly Cys Ala Ala Val Val Val	
555 560 565	
TGC GTC CGG CTG AAG CTA CAG AAA CAC CAG CCT CCA CCT GAA CCC TGT	1782
Cys Val Arg Leu Lys Leu Gln Lys His Gln Pro Pro Pro Glu Pro Cys	
570 575 580	
GGG GGA GAG ACA GAA ACC ATG AAC AAC CTA GCC AAT TGC CAG CGC GAG	1830
Gly Gly Glu Thr Glu Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu	
585 590 595	
AAG GAC GTT TCT GTT AGC ATC ATT GGG GCT ACC CAG ATC AAG AAC ACC	1878
Lys Asp Val Ser Val Ser Ile Ile Gly Ala Thr Gln Ile Lys Asn Thr	
600 605 610 615	
AAC AAG AAG GCG GAC TTT CAC GGG GAC CAT GGA GCC GAG AAG AGC AGC	1926
Asn Lys Lys Ala Asp Phe His Gly Asp His Gly Ala Glu Lys Ser Ser	
620 625 630	
TTT AAG GTC CGA TAC CCC ACT GTG GAC TAT AAC CTC GTT CGA GAC CTC	1974
Phe Lys Val Arg Tyr Pro Thr Val Asp Tyr Asn Leu Val Arg Asp Leu	
635 640 645	
AAG GGA GAT GAA GCC ACG GTC AGG GAT ACA CAC AGC AAA CGT GAC ACC	2022
Lys Gly Asp Glu Ala Thr Val Arg Asp Thr His Ser Lys Arg Asp Thr	
650 655 660	
AAG TGC CAG TCA CAG AGT CTG CAG GAG AAG AGA AGA TCG CCC CAA CAC	2070
Lys Cys Gln Ser Gln Ser Leu Gln Glu Lys Arg Arg Ser Pro Gln His	
665 670 675	

TTA GGG GTG GGG AGA TTC CTG ACA GAA AAC AGG CCA GAG TCT GTC TAC	2118
Leu Gly Val Gly Arg Phe Leu Thr Glu Asn Arg Pro Glu Ser Val Tyr	
680 685 690 695	
TCT ACT TCA AAG GAC ACC AAG TAC CAG TCG GTG TAT GTT CTG TCT GCA	2166
Ser Thr Ser Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Leu Ser Ala	
700 705 710	
GAA AAG GAT GAG TGT GTT ATA GCG ACT GAG GTG TAAGATGGAA GCGATGTGGC	2219
Glu Lys Asp Glu Cys Val Ile Ala Thr Glu Val	
715 720	
AAAATTCCCA TTTCTCTTAA ATAAAATTCC AAGGATATAG CCCCAGATGAA TGCTGCTGAG	2279
AGAGGAAGGG AGAGGAAACC CAGGGACTGC TGCTGAGAAC CAGGTTTCAGG CGAACGTGGT	2339
TCTCTCAGAG TTAGCAGAGG CGCCCGACAC TGCCAGCCTA GGCTTTGGCT GCCGCTGGAC	2399
TGCCTGCTGG TTGTTCCCAT TGCACATATGG ACAGTTGCTT TGAAGAGTAT ATATTTAAAT	2459
GGACGAGTGA CTTGATTTCAT ATAGGAAGCA CGCACTGCCC ACACGTCTAT CTTGGATTAC	2519
TATGAGCCAG TCTTTCCTTG AACTAGAAAC ACAACTGCCT TTATTGTCCT TTTTGATACT	2579
GAGATGTGTT TTTTTTTTTT CCTAGACGGG AAAAAAGAAAA CGTGTGTTAT TTTTTTTGGG	2639
ATTTGTAAAA ATATTTTTCAT TGATTATGGG AGAGCTCCCA ACGCGTTGGA GGT	2692

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Arg Arg Ser Ala Leu Ala Leu Ala Val Val Ser Ala Leu Leu	
1 5 10 15	
Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe	
20 25 30	
Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly	
35 40 45	
Ser Gly Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu Lys	
50 55 60	
His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser	
65 70 75 80	
Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly	
85 90 95	
Ala Gly Ile Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly	
100 105 110	
Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr	
115 120 125	
Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser	
130 135 140	
Arg Leu Thr Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser Gln	
145 150 155 160	
Asp Leu His Ser Ser Gly Arg Thr Asp Leu Arg Tyr Ser Tyr Arg Phe	
165 170 175	
Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys Arg	
180 185 190	

Pro	Arg	Asp	Asp	Ala	Phe	Gly	His	Phe	Thr	Cys	Gly	Asp	Arg	Gly	Glu
		195					200					205			
Lys	Met	Cys	Asp	Pro	Gly	Trp	Lys	Gly	Gln	Tyr	Cys	Thr	Asp	Pro	Ile
	210					215					220				
Cys	Leu	Pro	Gly	Cys	Asp	Asp	Gln	His	Gly	Tyr	Cys	Asp	Lys	Pro	Gly
225					230					235					240
Glu	Cys	Lys	Cys	Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu	Cys
				245					250					255	
Ile	Arg	Tyr	Pro	Gly	Cys	Val	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp	Gln
			260					265					270		
Cys	Asn	Cys	Gln	Glu	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp	Leu
		275					280					285			
Asn	Tyr	Cys	Thr	His	His	Lys	Pro	Cys	Arg	Asn	Gly	Ala	Thr	Cys	Thr
	290					295					300				
Asn	Thr	Gly	Gln	Gly	Ser	Tyr	Thr	Cys	Ser	Cys	Arg	Pro	Gly	Tyr	Thr
305					310					315					320
Gly	Ala	Asn	Cys	Glu	Leu	Glu	Val	Asp	Glu	Cys	Ala	Pro	Ser	Pro	Cys
				325					330					335	
Lys	Asn	Gly	Ala	Ser	Cys	Thr	Asp	Leu	Glu	Asp	Ser	Phe	Ser	Cys	Thr
			340					345					350		
Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Lys	Val	Cys	Glu	Leu	Ser	Ala	Met	Thr
		355					360					365			
Cys	Ala	Asp	Gly	Pro	Cys	Phe	Asn	Gly	Gly	Arg	Cys	Ser	Asp	Asn	Pro
	370					375					380				
Asp	Gly	Gly	Tyr	Thr	Cys	His	Cys	Pro	Leu	Gly	Phe	Ser	Gly	Phe	Asn
385					390					395					400
Cys	Glu	Lys	Lys	Met	Asp	Leu	Cys	Gly	Ser	Ser	Pro	Cys	Ser	Asn	Gly
				405					410					415	
Ala	Lys	Cys	Val	Asp	Leu	Gly	Asn	Ser	Tyr	Leu	Cys	Arg	Cys	Gln	Ala
			420					425					430		
Gly	Phe	Ser	Gly	Arg	Tyr	Cys	Glu	Asp	Asn	Val	Asp	Asp	Cys	Ala	Ser
			435				440					445			
Ser	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	Arg	Asp	Ser	Val	Asn	Asp	Phe
	450				455						460				
Ser	Cys	Thr	Cys	Pro	Pro	Gly	Tyr	Thr	Gly	Lys	Asn	Cys	Ser	Ala	Pro
465					470					475					480
Val	Ser	Arg	Cys	Glu	His	Ala	Pro	Cys	His	Asn	Gly	Ala	Thr	Cys	His
				485					490					495	
Gln	Arg	Gly	Gln	Arg	Tyr	Met	Cys	Glu	Cys	Ala	Gln	Gly	Tyr	Gly	Gly
			500					505					510		
Pro	Asn	Cys	Gln	Phe	Leu	Leu	Pro	Glu	Pro	Pro	Pro	Gly	Pro	Met	Val
		515					520					525			
Val	Asp	Leu	Ser	Glu	Arg	His	Met	Glu	Ser	Gln	Gly	Gly	Pro	Phe	Pro
	530					535					540				
Trp	Val	Ala	Val	Cys	Ala	Gly									

Thr	His	Ser	Lys	Arg	Asp	Thr	Lys	Cys	Gln	Ser	Gln	Ser	Leu	Gln	Glu
			660					665					670		
Lys	Arg	Arg	Ser	Pro	Gln	His	Leu	Gly	Val	Gly	Arg	Phe	Leu	Thr	Glu
		675					680					685			
Asn	Arg	Pro	Glu	Ser	Val	Tyr	Ser	Thr	Ser	Lys	Asp	Thr	Lys	Tyr	Gln
	690					695					700				
Ser	Val	Tyr	Val	Leu	Ser	Ala	Glu	Lys	Asp	Glu	Cys	Val	Ile	Ala	Thr
705					710					715					720
Glu	Val														

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Gly	Arg	Leu	Leu	Ala	Ser	Ala	Leu	Leu	Cys	Val	Ser	Gly	Val	Phe
1				5					10					15	
Glu	Leu	Lys	Leu	Gln	Glu	Phe	Val	Asn	Lys	Lys	Gly	Leu	Leu	Asn	Arg
			20					25					30		
Asn	Cys	Cys	Arg	Gly	Gly	Gly	Cys	Cys	Thr	Phe	Phe	Arg	Val	Cys	Leu
		35					40					45			
Lys	His	Tyr	Gln	Ala	Ser	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr	Tyr	Gly
	50					55					60				
Ser	Ala	Thr	Pro	Val	Leu	Gly	Ser	Phe	Ser	Pro	Asp	Gly	Ala	Gly	Asp
65					70					75					80
Pro	Ala	Phe	Ser	Asn	Pro	Ile	Arg	Phe	Pro	Phe	Gly	Phe	Thr	Trp	Pro
				85					90					95	
Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Leu	His	Thr	Asp	Ser	Pro	Asp
			100					105					110		
Asp	Leu	Thr	Glu	Asn	Pro	Glu	Arg	Leu	Ile	Ser	Arg	Leu	Thr	Gln	Arg
	115						120					125			
His	Leu	Val	Gly	Glu	Glu	Trp	Ser	Gln	Asp	Leu	His	Ser	Ser	Gly	Arg
	130					135					140				
Thr	Asp	Leu	Tyr	Ser	Tyr	Arg	Phe	Val	Cys	Asp	Glu	His	Tyr	Tyr	Gly
145					150					155					160
Glu	Gly	Cys	Ser	Val	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Phe	Gly	His	Phe
				165					170					175	
Thr	Cys	Gly	Arg	Gly	Glu	Lys	Cys	Pro	Gly	Trp	Lys	Gly	Gln	Tyr	Cys
			180					185					190		
Thr	Pro	Ile	Cys	Leu	Pro	Gly	Cys	Asp	Gln	His	Gly	Cys	Asp	Lys	Pro
		195					200					205			
Gly	Glu	Cys	Lys	Cys	Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu
	210					215					220				
Cys	Ile	Arg	Tyr	Pro	Gly	Cys	Val	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp
225					230					235					240
Gln	Cys	Asn	Cys	Gln	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp	
				245				250					255		
Leu	Asn	Tyr	Cys	Thr	His	His	Lys	Pro	Cys	Asn	Gly	Ala	Thr	Cys	Thr
			260					265					270		

Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr Thr
 275 280 285
 Gly Cys Glu Glu Glu Cys Pro Cys Lys Asn Gly Ser Cys Thr Asp Leu
 290 295 300
 Glu Ser Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Cys Glu Leu
 305 310 315 320
 Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys
 325 330 335
 Asp Asn Pro Asp Gly Gly Tyr Cys Cys Pro Leu Gly Ser Gly Phe Asn
 340 345 350
 Cys Glu Lys Lys Asp Cys Ser Ser Pro Cys Asn Gly Ala Cys Val Asp
 355 360 365
 Leu Gly Asn Ser Tyr Cys Cys Gln Ala Gly Phe Gly Arg Cys Asp Asn
 370 375 380
 Val Asp Asp Cys Ala Ser Pro Cys Asn Gly Gly Thr Cys Asp Val Asn
 385 390 395 400
 Asp Ser Cys Thr Cys Pro Pro Gly Tyr Gly Lys Asn Cys Ser Pro Val
 405 410 415
 Ser Arg Cys Glu His Pro Cys His Asn Gly Ala Thr Cys His Arg Arg
 420 425 430
 Tyr Cys Glu Cys Ala Gly Tyr Gly Gly Asn Cys Gln Phe Leu Leu Pro
 435 440 445
 Glu Pro Pro Gly Pro Val Asp Glu Glu Gln Phe Pro Trp Ala Val Cys
 450 455 460
 Ala Gly Leu Val Leu Leu Leu Gly Cys Ala Val Val Cys Val
 465 470 475 480
 Arg Leu Lys Gln Lys Pro Glu Cys Glu Thr Glu Thr Met Asn Asn Leu
 485 490 495
 Ala Asn Cys Gln Arg Glu Lys Asp Ser Ser Ile Gly Ala Thr Gln Ile
 500 505 510
 Lys Asn Thr Asn Lys Lys Asp Phe His Asp Lys Lys Val Arg Tyr Pro
 515 520 525
 Val Asp Tyr Asn Leu Val Leu Lys Val His Lys Lys Cys Ser Glu Glu
 530 535 540
 Lys Ala Leu Arg Lys Arg Pro Ser Val Tyr Ser Thr Ser Lys Asp Thr
 545 550 555 560
 Lys Tyr Gln Ser Val Tyr Val Ser Glu Lys Asp Glu Cys Ile Ala Thr
 565 570 575
 Glu Val

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACGATGAAY AACCTGGCGA ACTGCCAGCG TGAGAAGGAC ATCTCAGTCA GCATCATCGG	60
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG	120
TCCGACAAGA ATGGMTTTCA AGGCCCGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC	180
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG	240

TCCCCAGGCT	CCTCAGGGAG	GAGAAGGGGA	CCCCGACCAC	ACTCAGGGGK	TGCGTGCTGC	300
GGGCCGGGCT	CAGGAGGGGG	TACCTGGGGG	GTGTCTTCCT	GGAACCACTG	CTCCGTTTCT	360
CTTCCCAAAT	GTTCTCATGC	ATTCATTGTG	GATTTTCTCT	ATTTTCCTTT	TAGTGGAGAA	420
GCATCTGAAA	GAAAAAGGCC	GGACTCGGGC	TGTTCAACTT	CAAAAAGACAC	CAAGTACCAG	480
TCGGTGTACG	TCATATCCGA	GGAGAAGGAC	GAGTGCGTCA	TCGCA		525

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr	Asp	Glu	Xaa	Pro	Gly	Glu	Leu	Pro	Ala
1				5					10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu	Gly	His	Leu	Ser	Gln	His	His	Arg	Gly	Xaa	Val	Arg	Ser	Xaa	Thr
1				5					10					15	
Pro	Thr	Arg	Arg	Arg	Thr	Xaa	Xaa	Arg	Gly	Thr	Xaa	Ala	Ser	Asp	Lys
			20					25					30		
Asn	Gly	Phe	Gln	Gly	Pro	Leu	Pro	Gln	Arg	Gly	Leu				
		35					40								

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu	Val	Gln	Asp	Leu	Lys	Gly	Asp	Asp	Thr	Ala	Val	Arg	Thr	Ser	His
1				5					10					15	
Ser	Lys	Arg	Asp	Thr	Lys	Cys	Gln	Ser	Pro	Gly	Ser	Ser	Gly	Arg	Arg
			20					25				30			
Arg	Gly	Pro	Arg	Pro	His	Ser	Gly	Xaa	Ala	Cys	Cys	Gly	Pro	Gly	Ser
		35					40					45			

Gly	Gly	Gly	Thr	Trp	Gly	Val	Ser	Ser	Trp	His	Cys	Ser	Val	Ser	Leu
50					55					60					
Pro	Lys	Cys	Ser	His	Ala	Phe	Ile	Val	Asp	Phe	Leu	Tyr	Phe	Pro	Phe
65					70				75						80
Ser	Gly	Glu	Ala	Ser	Glu	Arg	Lys	Arg	Pro	Asp	Ser	Gly	Cys	Ser	Thr
				85					90					95	
Ser	Lys	Asp	Thr	Lys	Tyr	Gln	Ser	Val	Tyr	Val	Ile	Ser	Glu	Glu	Lys
			100					105					110		
Asp	Glu	Cys	Val	Ile	Ala										
			115												

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr	Met	Asn	Asn	Leu	Ala	Asn	Cys	Gln	Arg	Glu	Lys	Asp	Ile	Ser	Val
1				5					10					15	
Ser	Ile	Ile	Gly	Ala	Thr	Ser	Asp	Gln	Glu	His	Gln	Gln	Glu	Gly	Gly
			20					25					30		
Leu	Xaa	Xaa	Gly	Gly	Pro	Xaa	Pro	Thr	Arg	Met	Xaa	Phe	Lys	Ala	Arg
			35				40					45			
Tyr	Pro	Ser	Val	Asp	Tyr	Asn	Ser	Cys	Arg	Thr	Ser	Arg	Val	Thr	Thr
	50					55				60					
Pro	Pro	Ser	Gly	Arg	Arg	Thr	Ala	Ser	Val	Thr	Pro	Ser	Ala	Ser	Pro
65					70					75					80
Gln	Ala	Pro	Gln	Gly	Glu	Gly	Asp	Pro	Asp	His	Thr	Gln	Gly	Xaa	
			85					90					95		
Arg	Ala	Ala	Gly	Arg	Ala	Gln	Glu	Gly	Val	Pro	Gly	Gly	Cys	Leu	Pro
			100					105					110		
Gly	Thr	Thr	Ala	Pro	Phe	Leu	Phe	Pro	Asn	Val	Leu	Met	His	Ser	Leu
			115				120					125			
Trp	Ile	Phe	Ser	Ile	Phe	Leu	Leu	Val	Glu	Lys	His	Leu	Lys	Glu	Lys
	130					135					140				
Gly	Arg	Thr	Arg	Ala	Val	Gln	Leu	Gln	Lys	Thr	Pro	Ser	Thr	Ser	Arg
145				150						155					160
Cys	Thr	Ser	Tyr	Pro	Arg	Arg	Arg	Thr	Ser	Ala	Ser	Ser			
				165					170						

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Xaa Thr Trp Arg Thr Ala Ser Val Arg Arg Thr Ser Gln Ser Ala Ser
 1 5 10 15
 Ser Gly Xaa Arg Gln Ile Xaa Asn Thr Asn Lys Lys Ala Asp Phe Xaa
 20 25 30
 Xaa Gly Asp Xaa Ser Val Arg Gln Glu Trp Xaa Ser Arg Pro Ala Thr
 35 40 45
 Pro Ala Trp Thr Ile Thr Arg Ala Gly Pro Gln Gly
 50 55 60

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg His Arg Arg Gln Asp Val Ala Gln Gln Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His Gln Val Pro Val Pro Arg Leu Leu Arg Glu Glu Lys Gly Thr Pro
 1 5 10 15
 Thr Thr Leu Arg Gly Cys Val Leu Arg Ala Gly Leu Arg Arg Gly Tyr
 20 25 30
 Leu Gly Gly Val Phe Leu Glu Pro Leu Leu Arg Phe Ser Ser Gln Met
 35 40 45
 Phe Ser Cys Ile His Cys Gly Phe Ser Leu Phe Ser Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Lys Lys Ala Gly Leu Gly Leu Phe Asn Phe Lys Lys Arg His Gln
 1 5 10 15
 Val Pro Val Gly Val Arg His Ile Arg Gly Glu Gly Arg Val Arg His
 20 25 30
 Arg

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val
 1 5 10 15
 Ser Ile Ile Gly Ala Thr Gly Ile Xaa Asn Thr Asn Lys Lys Ala Asp
 20 25 30
 Phe Xaa Xaa Gly Asp Xaa Ser Ser Asp Lys Asn Gly Phe Gln Lys Ala
 35 40 45
 Arg Tyr Pro Ser Val Asp Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp
 50 55 60
 Asp Thr Ala Val Arg Thr Ser His Ser Lys Arg Asp Thr Lys Cys Gln
 65 70 75 80
 Ser Pro Gly Ser Ser Gly Arg Arg Arg Gly Pro Arg Pro His Ser Gly
 85 90 95
 Xaa Ala Cys Cys Gly Pro Gly Ser Gly Gly Gly Thr Trp Gly Val Ser
 100 105 110
 Ser Trp Asn His Cys Ser Val Ser Leu Pro Lys Cys Ser His Ala Phe
 115 120 125
 Ile Val Asp Phe Leu Tyr Phe Pro Phe Ser Gly Glu Ala Ser Glu Arg
 130 135 140
 Lys Arg Pro Asp Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr Gln
 145 150 155 160
 Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Val Ile Ala
 165 170 175

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2899 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCCAGCGGT	ACCATGGGCC	GTCTGGAGCGC	GCTACCCCTT	GCCGTGGTCT	CTGCCCTGCT	60
GTGCCAGGTC	TGGAGCTCCG	GCGTATTTGA	GCTGAAGCTG	CAGGAGTTCG	TCAACAAGAA	120
GGGGCTGCTG	GGGAACCGCA	ACTGCTGCCG	CGGGGGCTCT	GGCCCGCCTT	GCGCCTGCAG	180
GACCTTCTTT	CGCGTATGCC	TCAACCACTA	CCAGGCCAGC	GTGTCACCGG	AGCCACCCTG	240

CACCTACGGC	AGTGCTGTCA	CGCCAGTGCT	GGGTCTCGAC	TCCTTCAGCC	TGCCTSATKG	300
SGYASGSRYC	SMCCYCGAGG	YCKWCRGYAW	CSMYAAGYYY	GATATCGMMY	TYCGGCTTCA	360
CCTGGCCRRG	YACCTTCTCT	CTGATYATTG	AAGCYCTCCA	YACAGAYTCT	CCYGATGACC	420
TCGCAACAGA	AAACCCAGAA	AGACTCATCA	GCCGCCTGRC	CACYCAGAGG	CACCTSACKG	480
TGGMGARGA	RTGGTCYCAG	GACCTKCACA	GYAGCGGCCG	CACRGACCTC	MRGTACTCYT	540
ACCGSTTYGT	GTGTGACGAR	CACTACTACG	GAGARGGYTG	CTCTGTKTTC	TGCCGWCCYC	600
GGGAYGAYGC	CTTYGGCCAC	TTCACCTGYG	GGGASMGGWG	GGAGAARRTG	TGCRACCCCTG	660
GCTGGAAAGG	SCMGTAAGTC	ACWGASCCRA	TCTGYCTGCC	WGGRTGTGAT	GASCARCATG	720
GATWYTGTGA	CAAACCAAGG	GARTGCAAGT	GCAGAGTKGG	CTGGCAGGGC	CGSTACTGYG	780
ATGAGTGYAT	CCGYTAYCCA	GGYTGTCTCC	ATGGCACCTG	CCAGCARCCC	TGGCAGTGGA	840
ACTGCCAGGA	AGGNTGGGGG	GGCCTTTTCT	GCAACCARGA	CCTGAACTAC	TGYACWCACC	900
ATAAGCCSTG	CARGAATGGA	GCCACCTGCA	ACMAACACGG	GCCAGGGGGA	GCTACACWTG	960
KTCYTTGGCC	GGNCKYKGGG	AYANAGGGTG	CCAMCTGYGA	AGCTTGGGRA	KTRGAYGAGT	1020
TGTTGMYCCY	AGCCCYTGGY	AAGAACCAGG	SGAGCTKSAC	GGAYCTTCGG	AGRACAGCTW	1080
CTCYTGYACC	TGCCCWCCCG	GCTTCTAYGG	CAARRTCTGT	GARYTGAGYG	CCATGACCTG	1140
TGCRGAYGGC	CCTTGCTTYA	AYGGRGGWCG	RTGYTCAGAY	ARCCCYGAYG	GAGGSTACAS	1200
CTGCCRYTGC	CCCKTGGGCT	WCTCYGGCTT	CAACTGTGAG	AAGAARATKG	AYYWCTGCRG	1260
CTCTTCMCCY	TGTTCTAAYG	GTGCCAAGTG	TGTGGACCTC	GGYRAYKCYT	ACCTGTGCCG	1320
STGCCAGGCY	GGCTTCTCSG	GGAGGYACTG	YGASGACAA	GTGGAYGACT	GYGCCTCCTC	1380
CCCGTGYGCM	AAYGGGGGCA	CCTGCCGGGA	YRGYGTGAAC	GACTTGTCTC	GYACCTGCCC	1440
RCCTGGCTAC	ACGGGCARGA	ACTGCAGYGC	CCCYGYCAGC	AGGTGYGAGC	AYGCACCCTG	1500
CCAYAATGGG	GCCACCTGCC	ACSAGAGGGG	CCASCCTAY	WTGTGYGAGT	GYGCCRRRRG	1560
CTAYGGSGGY	CCCAACTGCC	ANTTYCTGCT	CCCYGAARCY	GMCCMCCMGG	SCCCAYGGTG	1620
GTGGAAMCTC	MSYKARARRM	AYMTARRAGR	GCCRGGGSGG	GCCCWTCCCC	TKGGTGGYCG	1680
TGTGYGCCGG	GGTSRTSCTT	GTCCTCMTGC	TGCTGCTGGG	CTGTGCTGCT	GTGGTGGTCT	1740
GCGTCCGGCT	GARGCTRCAG	AARCAACRGC	CYCCASCYGA	MCCCTGNSGG	GGRGAGACRG	1800
ARACCATGAA	CAACCTRGNC	AAATGCCAGC	GYGAGAAGGA	CRTYTCWGTY	AGCATCATYG	1860
GGGNYACSCA	CATCAAGAAC	ACCAACAAGA	AGGCGGACTT	YCACGGGGAC	CAYRGNGCCR	1920
ASAAGARYRG	CTTYAAGGYC	CGMTACCCMR	NKGTGGACTA	TAACCTCGTK	CRRGACCTCA	1980
AGGGWGAYGA	MRCRCRSGTC	AGGGAYRCRC	ACAGCAARCG	TGACACCAAG	TGNCAGYCMC	2040
AGRGCTCYKG	AGGRGARGAG	AAGGGGAYCS	CCGACCMACA	CTYAGGGGGT	GGAGGAAGMW	2100
TCYTGAMAGA	AAAAGGCCRG	ASTYYGGGY	TRYTCWACTT	TCAAARGACA	ANCMANGTAC	2160
MAGTCGGTGT	NYGTYMTKTC	YGNAGRAGGA	AGGNTGASTG	YGTYATAGGM	RNYTGAGGTN	2220
GTAARNTGGN	AGCGATGTGG	CAANNTTCCC	ATTCTCKSA	AAKNNNATTC	CMMGGATATA	2280
GCTCCGNTGA	ATGCTKCTGA	GAGAGGAAGG	GAGAGGAAAC	CCAGGGACTG	YTKYTCAGAA	2340
CCAGGTTTCA	GCGAAGCTGG	TTCTCTCAGA	GTTAGCAGAG	GCGCCCGACA	CTGCCAGCCT	2400
AGGCTTTGGC	TGCCGCTGGA	CTGCCCTGCT	GTTGTTCCCA	TTGCACTATG	GACAGTTGCT	2460
TTGAAGAGTA	TATATTTAAA	TGGACGAGTG	ACTTGATTCA	TATACGAAGC	ACGCACTGCC	2520
CACACGTCTA	TCTTGGATTA	CTATGAGCCA	GTCTTTTCTT	GAACCTAGAAA	CACAACTGCC	2580
TTTATTGTCC	TTTTTGTATC	TGAGATGTGT	TTTTTTTTTT	CCTAGACGGG	AAAAAGAAAA	2640
CGTGTGTTAT	TTTTTGTGGA	TTTGTAAGAA	TATTTTTCAT	GATATCTGTA	AAGCTTGAGT	2700
ATTTTGTGAC	GTTTATTTTT	TTATAATTTA	AATTTTGGTA	AATATGTACA	AAGGCACTTC	2760
GGGTCTATGT	GACTATATTT	TTTTGTATAT	AAATGTATTT	ATGGAATATT	GTGCAATATG	2820
TATTTGAGTT	TTTTACTGTT	TTGTTAATGA	AGAAATTCAT	TTTAAAAATA	TTTTTCCAAA	2880
ATAAATATAA	TGAACCTACA					2899

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu Lys Asp Glu Cys Val Ile Ala
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG 60
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA 120
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT 180
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAAGTA 240
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG 300
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA 360
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA 420
GCATGGATTT TGTGACAAAC CAGGGGAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA 480
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA 540
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC 600
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC 660
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA 720
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC 780
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG 840
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTGCGTGCT CAGACAGCCC CGATGGAGGG 900
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC 960
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG 1020
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC 1080
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCTGCACC 1140
TGCCCGCCTG GCTACACGGG CAGGAACGAG AGTGGCCCCG CCAGCAGGTG CGAGCACGCA 1200
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATTTGTG CGAGTGTGCC 1260
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AAAGTGGCCC CCGGCCCCCA 1320
CGGTGGTGGG AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT 1380
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTG CCGCTGTGGT 1440
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA 1500
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT 1560
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG 1620
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA 1680
CCTCAAGGGT GACGACACCG CCGTCAGGGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA 1740
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCGAC CCACACTCAG GGGGTGGAGG 1800
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTT AACTTTCAAA AGACAANCAA 1860
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG 1920
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCG GATTCCGNTT TCAAAGTTTT 1980
T 1981

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

His	Trp	Val	Arg	Ala	Pro	Leu	Glu	Val	Asp	Gly	Ile	Asp	Lys	Leu	Asp
1				5					10					15	
Ile	Glu	Phe	Arg	Leu	His	Leu	Ala	Gly	His	Leu	Leu	Ser	Asp	Tyr	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser	Ser	Pro	His	Arg	Phe	Ser
1				5		

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro	Arg	Asn	Arg	Lys	Pro	Arg	Lys	Thr	His	Gln	Pro	Pro	Gly	His	Pro
1				5					10					15	
Glu	Ala	Pro	Asp	Gly	Gly	Arg	Gly	Val	Val	Pro	Gly	Pro	Ala	Gln	Gln
			20					25					30		
Arg	Pro	His	Gly	Pro	Gln	Val	Leu	Leu	Pro	Leu	Arg	Val			
			35				40				45				

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg	Thr	Leu	Leu	Arg	Arg	Gly	Leu	Leu	Arg	Phe	Pro	Ser	Pro	Gly	Arg
1				5					10					15	

Cys Leu Arg Pro Leu His Leu Trp Gly Ala Trp Gly Glu Ser Val Gln
 20 25 30
 Pro Trp Leu Glu Arg Ala Leu His Arg Ala Asp Leu Pro Ala Trp
 35 40 45
 Met

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Ala Trp Ile Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Thr Arg Gly Met Gln Val Gln Ser Gly Leu Ala Gly Pro Val Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Val Tyr Pro Leu Ser Arg Leu Ser Pro Trp His Leu Pro Ala Ala
 1 5 10 15
 Leu Ala Val Gln Leu Pro Gly Arg Xaa Gly Gly Pro Phe Leu Gln Pro
 20 25 30
 Gly Pro Glu Leu Leu His Thr Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala	Leu	Gln	Glu	Trp	Ser	His	Leu	Gln	Gln	Thr	Arg	Ala	Arg	Gly	Ser
1				5					10					15	
Tyr	Thr	Trp	Ser	Leu	Ala	Gly	Leu	Gly	Tyr	Xaa	Gly	Cys	His	Leu	Arg
			20					25					30		
Ser	Leu	Gly	Ile	Gly	Arg	Val	Val	Asp	Pro	Ser	Pro	Trp			
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu	Arg	Arg	Glu	Leu	Asp	Gly	Ser	Ser	Glu	Asn	Ser	Tyr	Ser	Cys	Thr
1				5					10					15	
Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Lys	Ile	Cys	Glu	Leu	Ser	Ala	Met	Thr
			20					25					30		
Cys	Ala	Asp	Gly	Pro	Cys	Phe	Asn	Gly	Gly	Arg	Cys	Ser	Asp	Pro	Asp
		35					40					45			
Gly	Gly	Tyr	Ser	Cys	Arg	Cys	Pro	Val	Gly	Tyr	Ser	Gly	Phe	Asn	Cys
		50				55					60				
Glu	Lys	Lys	Ile	Asp	Tyr	Cys	Ser	Ser	Ser	Pro	Cys	Ser	Asn	Gly	Ala
				70						75				80	
Lys	Cys	Val	Asp	Leu	Gly	Asp	Ala	Tyr	Leu	Cys	Arg	Gly	Gln	Ala	Gly
			85						90				95		
Phe	Ser	Gly	Arg	His	Cys	Asp	Asp	Asn	Val	Asp	Asp	Cys	Ala	Ser	Ser
			100					105					110		
Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	Arg	Asp	Gly	Val	Asn	Asp	Phe	Ser
			115					120					125		
Cys	Thr	Cys	Pro	Pro	Gly	Tyr	Thr	Gly	Arg	Asn	Cys	Ser	Ala	Pro	Ala
			130			135					140				
Ser	Arg	Cys	Glu	His	Ala	Pro	Cys	His	Asn	Gly	Ala	Thr	Cys	His	Glu
				150						155				160	
Arg	Gly	His	Arg	Tyr	Xaa	Cys	Glu	Cys	Ala	Arg	Ser	Tyr	Gly	Gly	Pro
				165					170					175	
Asn	Cys	Xaa	Phe	Leu	Leu	Pro	Glu	Thr	Ala	Pro	Pro	Ala	Pro	Arg	Trp
			180					185					190		
Trp	Lys	Leu	Pro												
			195												

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Asn Leu Lys Gly Pro Gly Gly Ala His Pro Leu Gly Gly Arg Val
1 5 10 15
Arg Arg Gly His Pro Cys Pro His Ala Ala Ala Gly Leu Cys Arg Cys
20 25 30
Gly Gly Leu Arg Pro Ala Glu Ala Ala Glu Ala Pro Ala Pro Ser Arg
35 40 45
Pro Leu Xaa Gly Gly Asp Gly Asp His Glu Gln Pro Gly Gln Leu Pro
50 55 60
Ala
65

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Gly His Leu Ser Gln His His Arg Gly His Ala Asp Gln Glu His
1 5 10 15
Gln Gln Glu Gly Gly Leu Pro Arg Gly Pro Gln Xaa Arg Gln Glu Trp
20 25 30
Leu Gln Gly Pro Leu Pro Xaa Gly Gly Leu
35 40

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Pro Arg Ala Gly Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Arg His Arg Arg Gln Gly Arg Ala Gln Gln Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

His Gln Val Xaa Ala Pro Gly Leu Leu Arg Gly Gly Glu Gly Asp Pro
 1 5 10 15
 Arg Pro Thr Leu Arg Gly Trp Arg Lys His Leu Glu Arg Lys Arg Pro
 20 25 30
 Asp Phe Gly Leu Val Gln Leu Ser Lys Asp Xaa Gln Xaa Thr Ser Arg
 35 40 45
 Cys Xaa Ser Phe Pro Xaa Glu Glu Gly
 50 55

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Arg His Arg Xaa Leu Arg Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Xaa Trp Lys Xaa Xaa Pro Gly Phe Arg Phe Gln Ser Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ile Gly Tyr Gly Pro Pro Ser Arg Ser Thr Val Ser Ile Ser Leu Ile
1 5 10 15
Ser Asn Ser Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu
20 25 30
Ala Leu His Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu
35 40 45
Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu
50 55 60
Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr
65 70 75 80
Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser
85 90 95
Val Phe Cys Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly
100 105 110
Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys
115 120 125
Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys
130 135 140
Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr
145 150 155 160
Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln
165 170 175
Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys
180 185 190
Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly
195 200 205
Ala Thr Cys Asn Lys His Gly Pro Gly Gly Ala Thr Leu Gly Leu Trp
210 215 220
Pro Xaa Trp Gly Thr Xaa Gly Ala Thr Cys Glu Ala Trp Gly Leu Asp
225 230 235 240
Glu Leu Leu Thr Pro Ala Leu Gly Lys Asn Gly Gly Ser Leu Thr Asp
245 250 255
Leu Arg Arg Thr Ala Thr Pro Val Pro Ala His Pro Ala Ser Thr Ala
260 265 270
Lys Ser Val Asn
275

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Pro Val Arg Thr Ala Leu Ala Leu Thr Gly Val Gly Ala Gln Thr Ala
 1           5           10           15
Pro Met Glu Gly Thr Ala Ala Ala Ala Pro Trp Ala Thr Pro Ala Ser
          20          25          30
Thr Val Arg Arg Lys Leu Thr Thr Ala Ala Leu His Pro Val Leu Met
          35          40          45
Val Pro Ser Val Trp Thr Ser Val Met Pro Thr Cys Ala Ala Ala Arg
          50          55          60
Pro Ala Ser Arg Gly Gly Thr Val Thr Thr Thr Trp Thr Thr Ala Pro
65          70          75          80
Pro Pro Arg Ala Pro Thr Gly Ala Pro Ala Gly Met Ala
          85          90

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Thr Thr Ser Pro Ala Pro Ala Arg Leu Ala Thr Arg Ala Gly Thr Ala
 1           5           10           15
Val Pro Pro Pro Ala Gly Ala Ser Thr His Pro Ala Thr Met Gly Pro
          20          25          30
Pro Ala Thr Arg Gly Ala Thr Ala Ile Cys Ala Ser Val Pro Glu Ala
          35          40          45
Thr Gly Val Pro Thr Ala Xaa Ser Cys Pro Lys Leu Pro Pro Arg Pro
          50          55          60
His Gly Gly Gly Asn Ser Pro Lys Lys Thr
65          70

```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Lys Gly Arg Gly Gly Pro Ile Pro Leu Val Asp Val Cys Ala Gly Val
 1           5           10           15

```

Ile	Leu	Val	Leu	Met	Leu	Leu	Leu	Gly	Cys	Ala	Ala	Val	Val	Val	Cys
			20					25					30		
Val	Arg	Leu	Arg	Leu	Gln	Lys	His	Arg	Pro	Pro	Ala	Asp	Pro	Xaa	Arg
		35					40					45			
Gly	Glu	Thr	Glu	Thr	Met	Asn	Asn	Leu	Xaa	Asn	Cys	Gln	Arg	Glu	Lys
	50					55					60				
Asp	Ile	Ser	Val	Ser	Ile	Ile	Gly	Xaa	Thr	Gln	Ile	Lys	Asn	Thr	Asn
65					70					75					80
Lys	Lys	Ala	Asp	Phe	His	Gly	Asp	His	Ala	Asp	Lys	Asn	Gly	Phe	Lys
				85					90					95	
Ala	Arg	Tyr	Pro	Xaa	Val	Asp	Tyr	Asn	Leu	Val	Gln	Asp	Leu	Lys	Gly
			100					105					110		
Asp	Asp	Thr	Ala	Val	Arg	Asp	Ala	His	Ser	Lys	Arg	Asp	Thr	Lys	Xaa
		115					120					125			
Gln	Pro	Gln	Gly	Ser	Ser	Gly	Glu	Glu	Gly	Thr	Pro	Asp	Pro	His	Ser
	130					135					140				
Gly	Gly	Gly	Gly	Ser	Ile	Leu	Lys	Glu	Lys	Gly	Arg	Thr	Ser	Gly	Leu
145					150					155					160
Phe	Asn	Phe	Gln	Lys	Thr	Xaa	Xaa	Val	Gln	Val	Gly	Val	Arg	His	Phe
				165					170					175	
Arg	Arg	Arg	Lys	Xaa	Asp	Cys	Val	Ile	Gly	Xaa					
			180					185							

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly	Xaa	Lys	Xaa	Xaa	Val	Xaa	Xaa	Gly	Lys	Xaa	Ser	Pro	Asp	Ser	Xaa
1				5					10					15	
Phe	Lys	Val	Phe												
			20												

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu	Gly	Thr	Gly	Pro	Pro	Arg	Gly	Arg	Arg	Tyr	Arg
1				5				10			

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Tyr Arg Ile Pro Ala Ser Pro Gly Arg Ala Pro Ser Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Leu Lys Leu Ser Thr Gln Ile Leu Leu Met Thr Ser Gln Gln Lys
 1 5 10 15
 Thr Gln Lys Asp Ser Ser Ala Ala Trp Pro Pro Arg Gly Thr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Trp Ala Arg Ser Gly Pro Arg Thr Cys Thr Ala Ala Ala Arg
 1 5 10 15
 Thr Ser Ser Thr Pro Thr Ala Ser Cys Val Thr Asn Thr Thr Glu
 20 25 30
 Arg Ala Ala Pro Phe Ser Ala Val Pro Gly Thr Met Pro Ser Ala Thr
 35 40 45
 Ser Pro Val Cys Ser Val Gly Arg Lys Cys Ala Thr Leu Ala Gly Lys
 50 55 60
 Gly Pro Thr Ala Gln Ser Arg Ser Ala Cys Leu Asp Val Met Ser Ser
 65 70 75 80
 Met Asp Phe Phe Val Thr Asn Gln Asn Ala Ser Ala Glu Trp Ala Gly
 85 90 95
 Arg Ala Gly Thr Val Thr Ser Val Ser Ala Ile Gln Ala Val Ser Met
 100 105 110
 Ala Pro Ala Ser Ser Pro Gly Ser Ala Thr Ala Arg Lys Xaa Gly Gly
 115 120 125

Ala Phe Ser Ala Thr Arg Thr
130 135

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Thr	Thr	Ala	His	Thr	Ile	Ser	Pro	Ala	Arg	Met	Glu	Pro	Pro	Ala	Thr
1				5					10					15	
Asn	Thr	Gly	Gln	Gly	Glu	Leu	His	Leu	Val	Phe	Gly	Arg	Xaa	Gly	Val
			20					25					30		
Xaa	Arg	Val	Pro	Pro	Ala	Lys	Leu	Gly	Asp	Trp	Thr	Ser	Cys		
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro	Gln	Pro	Leu	Val	Arg	Thr	Glu	Gln	Glu
1			5				10		

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Arg	Ile	Phe	Gly	Glu	Gln	Leu	Leu	Leu	Tyr	Leu	Pro	Thr	Arg	Leu	Leu
1				5					10				15		
Arg	Gln	Asn	Leu												
			20												

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ile Glu Cys His Asp Leu Cys Gly Arg Pro Leu Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Gly Ser Val Leu Arg Gln Pro Arg Trp Arg Val Gln Leu Pro Leu
 1 5 10 15
 Pro Arg Gly Leu Leu Arg Leu Gln Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Leu Leu Gln Leu Phe Thr Leu Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Trp Cys Gln Val Cys Gly Pro Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Cys	Leu	Pro	Val	Pro	Leu	Pro	Gly	Arg	Leu	Leu	Gly	Glu	Ala	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg	Gln	Arg	Gly	Arg	Leu	Arg	Leu	Leu	Pro	Val	Arg	Gln	Gly	His	Leu
1				5					10					15	
Pro	Gly	Trp	Arg	Glu	Arg	Leu	Leu	Leu	His	Leu	Pro	Ala	Trp	Leu	His
			20					25					30		
Gly	Gln	Glu	Leu	Gln	Cys	Pro	Arg	Gln	Gln	Val	Arg	Ala	Arg	Thr	Leu
		35				40					45				
Pro	Gln	Trp	Gly	His	Leu	Pro	Arg	Glu	Gly	Pro	Pro	Leu	Phe	Val	Arg
	50					55				60					
Val	Cys	Pro	Lys	Leu	Arg	Gly	Ser	Gln	Leu	Pro	Xaa	Pro	Ala	Pro	Arg
65				70					75						80
Asn	Cys	Pro	Pro	Gly	Pro	Thr	Val	Val	Glu	Thr	Pro	Leu	Lys	Lys	Pro
			85					90						95	
Lys	Arg	Ala	Gly	Gly	Gly	Pro	Ser	Pro	Trp	Trp	Thr	Cys	Ala	Pro	Gly
		100						105					110		
Ser	Ser	Leu	Ser	Ser	Cys	Cys	Cys	Trp	Ala	Val	Pro	Leu	Trp	Trp	Ser
		115					120					125			
Ala	Ser	Gly													
															130

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly	Cys	Arg	Ser	Thr	Gly	Pro	Gln	Pro	Thr	Pro	Xaa	Gly	Gly	Arg	Arg
1				5					10					15	
Arg	Pro														

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr	Thr	Trp	Xaa	Thr	Ala	Ser	Val	Arg	Arg	Thr	Ser	Gln	Ser	Ala	Ser
1				5					10					15	
Ser	Gly	Xaa	Arg	Arg	Ser	Arg	Thr	Pro	Thr	Arg	Arg	Arg	Thr	Ser	Thr
			20					25					30		
Gly	Thr	Thr	Xaa	Pro	Thr	Arg	Met	Ala	Ser	Arg	Pro	Ala	Thr	Gln	Xaa
		35					40					45			
Trp	Thr	Ile	Thr	Ser	Cys	Arg	Thr	Ser	Arg	Val	Thr	Thr	Pro	Pro	Ser
	50				55					60					
Gly	Thr	Arg	Thr	Ala	Ser	Val	Thr	Pro	Ser	Xaa	Ser	Pro	Arg	Ala	Pro
65				70					75					80	
Gln	Gly	Arg	Arg	Arg	Cys	Pro	Pro	Thr	His	Thr	Gln	Gly	Val	Glu	Glu
			85					90						95	
Ala	Ser														

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Lys	Lys	Lys	Ala	Gly	Leu	Arg	Ala	Cys	Ser	Thr	Phe	Lys	Arg	Gln	Xaa
1			5						10					15	
Xaa	Tyr	Lys	Ser	Val	Xaa	Val	Ile	Ser	Xaa	Gly	Gly	Arg	Xaa	Thr	Ala
			20					25					30		
Ser															

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Xaa Glu Val Val Xaa Trp Xaa Leu Xaa Leu Glu Xaa Xaa Pro Arg
1 5 10 15
Ile Pro Xaa Ser Lys Phe
20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His
1 5 10 15
Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile
20 25 30
Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Trp Ser
35 40 45
Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg
50 55 60
Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
65 70 75 80
Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
85 90 95
Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro
100 105 110
Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro
115 120 125
Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu
130 135 140
Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp
145 150 155 160
Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp
165 170 175
Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys
180 185 190

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr Asn Thr Gly Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Asn Gly Gly Ser Leu Thr Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu	Asn	Ser	Tyr	Ser	Cys	Thr	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Lys	Ile
1				5					10					15	
Cys	Glu	Leu	Ser	Ala	Met	Thr	Cys	Ala	Asp	Gly	Pro	Cys	Phe	Asn	Gly
		20						25					30		
Gly	Arg	Cys	Ser	Asp	Ser	Pro	Asp	Gly	Gly	Tyr	Ser	Cys	Arg	Cys	Pro
		35					40					45			
Val	Gly	Tyr	Ser	Gly	Phe	Asn	Cys	Glu	Lys	Lys	Ile	Asp	Tyr	Cys	Ser
	50					55					60				
Ser	Ser	Pro	Cys	Ser	Asn	Gly	Ala	Lys	Cys	Val	Asp	Leu	Gly	Asp	Ala
65					70					75					80
Tyr	Leu	Cys	Arg	Cys	Gln	Ala	Gly	Phe	Ser	Gly	Arg	His	Cys	Asp	Asp
			85						90					95	
Asn	Val	Asp	Asp	Cys	Ala	Ser	Ser	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys
			100					105					110		
Arg	Asp	Gly	Val	Asn	Asp	Phe	Ser	Cys	Thr	Cys	Pro	Pro	Gly	Tyr	Thr
		115					120					125			
Gly	Arg	Asn	Cys	Ser	Ala	Pro	Ala	Ser	Arg	Cys	Glu	His	Ala	Pro	Cys
	130					135					140				
His	Asn	Gly	Ala	Thr	Cys	His	Glu	Arg	Gly	His	Arg	Tyr			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Cys Glu Cys Ala Arg Ser Tyr Gly Gly Pro Asn Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Phe Leu Leu Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Pro Pro Gly Pro
1

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Leu Leu Gly Cys Ala Ala Val Val Val Cys Val Arg Leu Arg Leu
1 5 10 15
Gln Lys His Arg Pro Pro Ala Asp Pro
20 25

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Arg Gly Glu Thr Glu Thr Met Asn Asn Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val	Asp	Tyr	Asn	Leu	Val	Gln	Asp	Leu	Lys	Gly	Asp	Asp	Thr	Ala	Val
1				5					10					15	
Arg	Asp	Ala	His	Ser	Lys	Arg	Asp	Thr	Lys						
			20					25							

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gln	Pro	Gln	Gly	Ser	Ser	Gly	Glu	Glu	Lys	Gly	Thr	Pro
1				5					10			

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Pro	Thr	Leu	Arg
1			

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Arg Lys Arg Pro

1

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCGGNTTYA CNTGGCCNGG NAC

23

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

(A) NAME/KEY: Modified Base
(B) LOCATION: 12
(D) OTHER INFORMATION: N=Inosine

(A) NAME/KEY: Modified Base
(B) LOCATION: 15
(D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCNATGCANG TNCCNCCRTT

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Gly Phe Thr Trp Pro Gly Thr
1 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Asn Gly Gly Thr Cys Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Ser Ile Pro Pro Gly Ser Arg Thr Ser Leu Gly Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGNTTCACNT GGCCNGGNAC NTT

23

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTNCCNCCRT TYTTRCANGG RTT

23

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Asn Pro Cys Lys Asn Gly Gly Thr

1

5

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACNATGAAYA AYCTNGCNAA YTG

23

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Thr Met Asn Asn Leu Ala Asn Cys
1 5

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ACRTANACNG AYTGR TAYTT NGT

23

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Thr Lys Tyr Gln Ser Val Tyr Val
1 5

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Modified Base
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: N=Inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCDATNACRC AYTCTTCYTT YTC

23

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Gly Phe Thr Trp Pro Gly Thr Phe
 1 5